

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
 CCCGCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCCCTTGCTGACGGCGTCG
 AGCCCTGGCCAGACATGTCCACAGGGTTCTCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGCTAGACAA
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACCTA
 GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAATATGGAAC
 CCTGCAAGGAAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT
 TCTCCAGACTCCCTTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
 ATGTACGTGAGCACGCGGGAAACGGTACAAGTGCTGCGCTTCAGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCCGGCGCGCCCGGGGATCCCCAGCTGCCAGTGTGTTCTGGTTCC
 CGGAGGCGCCTTCATCGTGGGCGTGTCTTCTGTACAGAGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGCTGGTGTCTTCGACACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA
 CGACAGCCACGCGCGGGGAACCTGGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTG
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAATGTGACCTGTTCGGCCAGTCCGGC
 GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
 CATTTCCAGAGTGGCACCGGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAAGGTTGCCCACTGGCTGGATGCAACCAACAGCACACAGATTCCTGGTAAACTGC
 CTGAGGGCACTATCAGGGAACCAAGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAT
 GAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCTGTGGTGGATGGTGTGG
 TGATCCAGAGTACCCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATACCAAGGAGCAGGT
 ACCACTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGTCTAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGGAAGCTCAAGGAGAAGAAGATGGC
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCCAATTCTAAGGGTGGC
 TATGCAGGAGGAGGCCAAAGAGGGGTTTGGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACTGGGCAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCAGTGCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTTCAAATCCT
 CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACACCGAGCTGCCACTGC
 CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGTCAACCTTGTTCCTGTCTGT
 TCACATTGGCCCTTGGAGCCTTGGCAGGTTGTGACATGGAGCAAACTTTTGTAGTTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCAAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAAGAGTGTGATTAGAAAAA

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FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTQGKQMHVGKTPIQVFLGVPPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGW\$LALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWQGLASMYVSTRERYKWLRFSEDCLYLNVAAPARAPGDPQLPVMVWVFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPETIIWSMSPVVDGVVIPPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGTCT
 GCTGTCTCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
 AGTCAGTGTATGGTCCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGGA
 CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGA CTGAGACAAC
 CAAGGGTGCTCCTGTGGGCCAACACCACAGAGTCGAGAGGTGGAATGAGCACCCGGGGCC
 GATTCCAGCTCACTGGGGATCCGCCAAGGGGAACCTGCTCCTTGGTGTATCAGAGACGCGCAG
 ATGACAGGATGAGTCACTACTTCTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
 CATGAACGATGGGTTCTTTCTAAAGTAACAGTGTCTCAGCTTACGCCAGACCCAGGACC
 ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
 GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTACGTGACAACAC
 GCCAGCCTGGAGCCCCAGCCCCAGGGAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT
 TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAG
 AACAGAGTCTCTCTCTGCTCCATCCTTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
 GGTGAAGGCTGGGGATTCAAGGCGCTACACCTGCCAGCGGAGAACAGGCTTGGCTCCAGC
 AGCGAGCCTTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
 GCAACAGGACAGTCTTGGAAAACTTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCA
 AAGCCTGTGCTGGTCTGTGTGTCACACAGCAGCCCCCAGCGCTGAGCTGGACCCAGGA
 GGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGTCTCTGGAGCTGCTTCCGGTT
 CAACTGGAGCACGAAGGAGAGTTCACTTGCCACGCTCGGCCACTGGGCTCCAGCAGCT
 CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
 CGTTTTCTGGGAATCGGCATCAGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG
 ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
 GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
 AAGCCACACCAACAGTCTCGGACCCCTCCTCCACAGGCTGCTCCTCCCAAGATCAAAG
 AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCTCACTCAAGC
 CCCAGAATCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCA
 GACCCAGGCTGAGGCCCGGATGCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
 CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
 GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTTTCTCTCTCTCT
 CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGCGACAGTGGCTCACGCCTGTAATC
 CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCTGAGGTGCGGAGTTGCGACACGACCTG
 GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCACTGGTGGCAGG
 CGCCTGTAATCCTACTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
 AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
 TCTCAAAAAAAATCCTCCAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
 AGGTGGGTGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC
 ATCTCTCAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCAGCTGT
 CAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
 TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCAAGGATGAGACAGGAGGTCCG
 TACAAGATACAGGTCAATAAGACTTTGCTGATAAAAACAGATTGCACTAAAGAAGGCCAACCA
 ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCTACTGTACACTCCT
 GCAGACCACTCAGAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
 AAAGGGGAGGAATGAATAATCCACCCCTTGTGTAGCAATAAGCAAGAAATAACCATAAAA
 GTGGGCAACAGCAGCTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTCTCTT
 TACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

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